



## SEQUENCE LISTING

<110> Junghans, Richard P.

<120> Antibodies as Chimeric Effector Cell Receptors Against Tumor Antigen

<130> 003

<140> 10/066,773

<141> 2001-10-12

<150> 60/250,089

<151> 2000-11-30

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 7654

<212> DNA

<213> Homo sapiens and Mus sp.

<220>

<221> CDS

<222> (2428)..(3759)

<223> Chimeric IgTCR sequence contained in retroviral vector. Retroviral vector sequence (non-coding regions) are incidental to the invention. The translated (coding region) is relevant to the invention. (pertinent to Figure 3.)

<400> 1	60
aagcttgcattgcgttgcagggtcgactctaggcacataaagaaaaacataaacataaccgt	120
gcagccgaga cagtgaaaag aaccgttaaa acggtttggttttaaataaac tgaattatttt	180
agagtcattt ctttggtagg aaagtacatt ggcacgtaaa ggagccaaa gcaatctgtg	240
gaaagcccaag gctgggagcc cagcagtttgcattccctcc tggcgtgtac ctaagggttt	300
cttaattgttgcgttgcaggat atcttccaga gggtttgcgttgcattcacttcacttcgttgc	360
cacaatactt ggacgcggat ttactgttgcgttgcattcacttcacttcacttcgttgc	420
tgaacctgag gcccaacttcttcagcttgcgttgcaggagagca caagcaccag aagaggctga	

cccgccagac ctgtggcat tttacaag ggcctcctgg gtctgtggga ggcaggctta	480
cataaggtgc aaattagaaa tataaataat aagccatata caatttgtca tctttttta	540
agctcaagtt ttgaaagacc ccacctgttag gtttggcaag ctagcttaag taacgccatt	600
ttgcaaggca tggaaaatac ataactgaga atagagaagt tcagatcaag gtttaggaaca	660
gagagacagc agaatatggg ccaaacagga tatctgtggt aagcagttcc tgccccgctc	720
agggccaaga acagttggaa caggagaata tggccaaac aggatatctg tggtaagcag	780
ttcctgcccc ggctcaggc caagaacaga tggtccccag atgcggtccc gccctcagca	840
gtttctagag aaccatcaga tggccagg gtgccccaaag gacctgaaat gaccctgtgc	900
cttatttcaa ctaaccaatc agtcgcttc tcgcttctgt tcgcgcgcctt ctgctccccg	960
agctcaataa aagagccac aaccctcac tcggcgcgcc agtcctccga tagactgcgt	1020
cgtccggta cccgtattcc caataaagcc tcttgctgtt tgcattccaa tcgtggactc	1080
gctgatcctt gggagggctt cctcagattt attgactgcc cacctcgggg gtcttcatt	1140
tggaggttcc accgagattt ggagacccct gcccaggac caccgacccc cccgcccggaa	1200
ggtaagctgg ccagcaactt atctgtgtct gtccgattgt ctatgtctta tgactgattt	1260
tatgcgcctg cgtcggtact agttagctaa ctatgtctgt atctggcgaa cccgtgggtgg	1320
aactgacgag ttccgaacac ccggccgcaa ccctggaga cgtcccaggg acttcgggggg	1380
ccgtttttgt ggcccgcactt gagtcctaaa atcccgatcg tttaggactc ttgggtgcac	1440
cccccttaga ggagggatat gtgggtctgg taggagacga gaacctaaaa cagttccgc	1500
ctccgtctga atttttgcctt tcgggttggg accgaagccg cggcgcgcgt ctgtctgt	1560
gcagcatcgatctgtgt ctatgtctga ctatgtttctgt gtatgttgcataaaatatgg	1620
gcccgggcta gactgttacc actccctaa gtttgcaccc aggtcactgg aaagatgtcg	1680
agcggatcgc tcacaaccag tcggtagatg tcaagaagag acgttgggtt accttctgt	1740
ctgcagaatg gccaaccttt aacgtcgat ggcgcgaga cggcacctt aaccgagacc	1800
tcatcaccca ggttaagatc aaggtctttt cacctggccc gcatggacac ccagaccagg	1860

tcccctacat cgtgacacctgg	gaagccttgg	ctttgaccc	ccctccctgg	gtcaagccct	1920
ttgtacaccc	taagcctccg	cctcctcttc	ctccatccgc	cccgctcttc	1980
ctcctcggttc	gaccccgctt	cgatcctccc	tttatccagc	cctcactcct	2040
ccccatatg	gccatatgag	atcttatatg	gggcacccccc	gccccttgta	2100
accctgacat	gacaagagtt	actaacagcc	cctctctcca	agtcactta	2160
cttagtccag	cacgaagtct	ggagacctct	ggcggcagcc	taccaagaac	2220
accggtgtta	cctcaccctt	accgagtcgg	cgacacagtg	tgggtccgcc	2280
taagaaccta	gaacctcgct	ggaaaggacc	ttacacagtc	ctgctgacca	2340
cctcaaagta	gacggcatcg	cagttggat	acacgcccgc	cacgtgaagg	2400
cgggggtgga	ccatcctcta	gactgcc	atg gga tgg	agc tgt atc atc	2454
			Met Gly Trp	Ser Cys Ile Ile Leu Phe	
			1	5	
ttg gta gca aca gct aca ggt gtc	cac tcc gac atc cag	ctg acc cag			2502
Leu Val Ala Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln					
10	15	20	25		
agc cca agc agc ctg agc gcc agc gtg ggt gac aga	gtg acc atc acc				2550
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr					
30	35	40			
tgt aag gcc agt cag gat gtg ggt act tct gta gct tgg	tac cag cag				2598
Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln					
45	50	55			
aag cca ggt aag gct cca aag ctg ctg atc tac tgg	aca tcc acc cgg				2646
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg					
60	65	70			
cac act ggt gtg cca agc aga ttc agc ggt agc ggt acc gac					2694
His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp					
75	80	85			
ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gcc acc tac					2742
Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr					
90	95	100	105		
tac tgc cag caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag					2790
Tyr Cys Gln Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys					

	110	115	120	
gtg gaa atc aaa cga ggt ggc tca gga tcg ggt gga tcc ggc tct ggt Val Glu Ile Lys Arg Gly Gly Ser Gly Ser Gly Ser Gly Ser Gly	125	130	135	2838
ggc tca gga tcg gag gtc caa ctg gtg gag agc ggt gga ggt gtt gtg Gly Ser Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Val Val	140	145	150	2886
caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc gat Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp	155	160	165	2934
ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa ggt Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly	170	175	180	2982
ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac tat Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr	190	195	200	3030
gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc aag Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys	205	210	215	3078
aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc ggg Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly	220	225	230	3126
gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct tat Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr	235	240	245	3174
tgg ggc caa ggg acc ccg gtc acc gtc tcc agt gct aag ccc acc acg Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Lys Pro Thr Thr	250	255	260	3222
acg cca gcg ccg cga cca cca aca ccg gcg ccc acc atc tcg cag Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln	270	275	280	3270
ccc ctg tcc ctg cgc cca gag gcg gct cggt cca gcg gcg ggg ggc gca Pro Leu Ser Leu Arg Pro Glu Ala Ala Arg Pro Ala Ala Gly Gly Ala	285	290	295	3318
gtg cac acg agg ggg ctg gac ttc gcc ctg gat ccc aaa ctc tgc tac Val His Thr Arg Gly Leu Asp Phe Ala Leu Asp Pro Lys Leu Cys Tyr				3366

300	305	310	
ctg ctg gat gga atc ctc ttc atc tat ggt gtc att ctc act gcc ttg Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu 315	320	325	3414
ttc ctg aga gtg aag ttc agc agg agc gca gag ccc ccc gcg tac cag Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln 330	335	340	3462
cag ggc cag aac cag ctc tat aac gag ctc aat cta gga cga aga gag Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu 350	355	360	3510
gag tac gat gtt ttg gac aag aga cgt ggc cgg gac cct gag atg ggg Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly 365	370	375	3558
gga aag ccg aga agg aag aac cct cag gaa ggc ctg tac aat gaa ctg Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu 380	385	390	3606
cag aaa gat aag atg gcg gag gcc tac agt gag att ggg atg aaa ggc Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly 395	400	405	3654
gag cgc cgg agg ggc aag ggg cac gat ggc ctt tac cag ggt ctc agt Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser 410	415	420	3702
aca gcc acc aag gac acc tac gac gcc ctt cac atg cag gcc ctg ccc Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro 430	435	440	3750
cct cgc taa ctcgacgcgg ccgcggatcc ggatttagtcc aatttgttaa Pro Arg			3799
agacaggata tcagtggtcc aggctctagt tttgactcaa caatatcacc agctgaagcc			3859
tatagagtac gagccataga taaaataaaa gattttattt agtctccaga aaaagggggg			3919
aatgaaaagac cccacctgta ggtttggcaa gctagcttaa gtaacgccat tttgcaaggc			3979
atggaaaata cataactgag aatagagaag ttcagatcaa ggttaggaac agagagacag			4039
cagaatatgg gccaaacagg atatctgtgg taagcagttc ctgccccgct cagggccaag			4099

aacagttgga acaggagaat atgggc当地 caggatatct gtggtaagca gttc当地 gccc	4159
cggctc当地 ggg ccaagaacag atggtccccca gatgc当地 gtc cgc当地 cagc agtttctaga	4219
gaaccatcag atgtttccag ggtgccccaa ggacctgaaa tgaccctgtg ccttatttga	4279
actaaccat cagttcgctt ctc当地 tctg ttc当地 cgc当地 gct tctgctcccc gagctcaata	4339
aaagagccca caaccctca ctc当地 cgc当地 cagtc当地 cccg atagactgca tc当地 cccgggt	4399
acccgtgttc tcaataaaacc ctcttgc当地 tgc当地 cc当地 tc当地 ggtctc gctgttcc	4459
gggagggtct ctctgagtgta ttgactaccc gtc当地 cgggg tctttc当地 tctccac	4519
acacaggctc cactaacatt cctgatgtgc cgc当地 gggact cc当地 cagccca gtttttgtt	4579
tataataaaa tgcaagaaca gtgttccctt caagccagac tacatcctga ctctc当地 gg	4639
tataaaagaa ttttgaaggg ctctgtggac tatctgccac acgactttt aagattttt	4699
tgc当地 cctgg atgaggatt tagtcaatct atc当地 cgtct attttgc当地 cttctccgta	4759
ttttaaattt ctatgttgc当地 ctcccttc当地 gagagcacgg cgattgc当地 gtagttaata	4819
ctctgagggc aggcttctgt gaaaaggttg cctggctca gtgtgagatt ttgc当地 aaaa	4879
aagggtc当地 gccc当地 gtgt acagacagat cggaaatctag agtgc当地 tact cagatcccc	4939
gc当地 gttccgg ggctctgatc tc当地 ggc当地 tttgc当地 tagtgc当地 cttccgta	4999
tc当地 gggccgg gtaccgagct cgaattcgta atcatggta tagtgc当地 ctgtgtgaaa	5059
ttgttatccg ctc当地 cattt cacacaacat acgagccgga agcataaaatgt gtaaaggcctg	5119
gggtgc当地 aa tgagtgagct aactcacatt aattgc当地 cgctc当地 tactgc cc当地 cttcc	5179
gtc当地 gggaaac ctgtc当地 tgcc agctgc当地 ttaatgc当地 caacgc当地 cgg ggagaggcgg	5239
tttgc当地 tattt gggc当地 ctcc gcttccctc gctc当地 tactgc当地 tc当地 gtc当地 cgct	5299
gctgc当地 ggca gc当地 ggtatcag ctc当地 tactcaaa ggc当地 gtaata cggttatcca cagaatcagg	5359
ggataacgc当地 ggaaagaaca tgtgagcaaa aggccagca aaggccagga accgtaaaaaa	5419
ggccgc当地 gtttgc当地 ctggc当地 gttt tccataggct cc当地 cccct gacgagc当地 atcg	5479
acgctcaatgt cagaggtggc gaaaccgc当地 aggactataa agataccagg cgtttcccc	5539

tggaagctcc	ctcgtgcgct	ctcctgttcc	gaccctgccc	cttaccggat	acctgtccgc	5599
ctttctccct	tcgggaagcg	tggcgcttcc	tcatagctca	cgctgttaggt	atctcagttc	5659
ggtgttaggtc	gttcgctcca	agctgggctg	tgtgcacgaa	ccccccgttc	agcccgaccg	5719
ctgcgcctta	tccggtaact	atcgtcttga	gtccaacccg	gtaagacacg	.acttatcgcc	5779
actggcagca	gccactggta	acaggattag	cagagcgagg	tatgttaggcg	gtgctacaga	5839
gttcttgaag	tggtggccta	actacggcta	cactagaagg	acagtatttg	gtatctgcgc	5899
tctgctgaag	ccagttacct	tcggaaaaag	agttggtagc	tcttgcgtcc	gcaaacaaac	5959
caccgctgg	agcggtggtt	tttttggtt	caagcagcag	attacgcgca	aaaaaaaagg	6019
atctcaagaa	gatccttga	tctttctac	ggggtctgac	gctcagtgg	acgaaaaactc	6079
acgttaaggg	attttgtca	tgagattatc	aaaaaggatc	ttcacctaga	tcctttaaa	6139
ttaaaaatga	agttttaaat	caatctaaag	tatatatgag	taaacttgg	ctgacagtt	6199
ccaatgctta	atcagtgagg	cacctatctc	agcgatctgt	ctattcggt	catccatagt	6259
tgccctgactc	cccgctgtgt	agataactac	gatacggag	ggcttaccat	ctggccccag	6319
tgctgcaatg	ataccgcgag	acccacgctc	accggctcca	gatttatcag	caataaacca	6379
gccagccgga	agggccgagc	gcagaagtgg	tcctgcaact	ttatccgcct	ccatccagtc	6439
tattaattgt	tgccggaaag	ctagagtaag	tagttcgcca	gttaatagtt	tgcgcaacgt	6499
tgttgccatt	gctacaggct	cgtgggtca	cgctcgctgt	ttggtatggc	ttcattcagc	6559
tccggttccc	aacgatcaag	gcgagttaca	tgatccccca	tgttgtgcaa	aaaagcggtt	6619
agctccttcg	gtcctccgat	cgttgtcaga	agtaagttgg	ccgcagtgtt	atcactcatg	6679
gttatggcag	cactgcataa	ttctcttact	gtcatgccat	ccgtaagatg	ctttctgtg	6739
actggtgagt	actcaaccaa	gtcattctga	gaatagtgt	tgccggcacc	gagttgctct	6799
tgcccggcgt	caatacggga	taataccgcg	ccacatagca	gaactttaaa	agtgctcatc	6859
attggaaaac	gttcttcggg	gcgaaaaactc	tcaaggatct	taccgctgtt	gagatccagt	6919
tcgatgtaac	ccactcggtc	acccaactga	tcttcagcat	cttttacttt	caccagcggt	6979

tctgggtgag caaaaacagg aaggcaaaat gccgcaaaaa aggaaataag ggcgacacgg	7039
aaatgttcaa tactcatact cttcctttt caatattatt gaagcattta tcagggttat	7099
tgtctcatga gcggatacat atttgaatgt atttagaaaa ataaacaaat aggggttccg	7159
cgcacatttc cccgaaaagt gccacctgac gtctaagaaa ccattattat catgacatta	7219
acctataaaa ataggcgtat cacgaggccc ttgcgtctcg cgcgttcgg tgcgtacgg	7279
gaaaaacctct gacacatgca gctccggag acggtcacag cttgtctgt agcggatgcc	7339
gggagcagac aagccgtca gggcggtca gcgggtgttg gcgggtgtcg gggctggctt	7399
aactatgcgg catcagagca gattgtactg agagtgcacc atatgcggtg taaaataccg	7459
cacagatgcg taaggagaaa ataccgcattc aggccattcgcg cgtgcgcaac	7519
tgttggaaag ggcgatcggt gcgggcctct tcgctattac gccagctggc gaaaggggg	7579
tgtgctgcaa ggcgattaaag ttggtaacg ccagggtttt cccagtcacg acgttgtaaa	7639
acgacggcca gtgcc	7654

<210> 2

<211> 443

<212> PRT

<213> Homo sapiens and Mus sp.

<400> 2

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1															

Val	His	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala

Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val

Gly	Thr	Ser	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg  
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu  
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly  
115 120 125

Ser Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Ser Glu Val Gln  
130 135 140

Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg  
145 150 155 160

Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser  
165 170 175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile  
180 185 190

His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg  
195 200 205

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met  
210 215 220

Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu  
225 230 235 240

Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val  
245 250 255

Thr Val Ser Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro  
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu  
275 280 285

Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp  
290 295 300

Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe  
305 310 315 320

Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser  
325 330 335

Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr  
340 345 350

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys  
355 360 365

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn  
370 375 380

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu  
385 390 395 400

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Gly Lys Gly  
405 410 415

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr  
420 425 430

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
435 440

<210> 3  
<211> 504  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (6)..(425)  
<223> MB3.6 Heavy chain V region, plus leader

<400> 3	50
tcacc atg aac ttc ggg ttc agc ttg att ttc ctt gtc ctt gtt tta aaa	
Met Asn Phe Gly Phe Ser Leu Ile Phe Leu Val Leu Val Leu Lys	
1 5 10 15	
ggt gtc cag tgt gaa gtg gtg gtg gag tct ggg gga ggc ttc gtg	98
Gly Val Gln Cys Glu Val Val Val Glu Ser Gly Gly Phe Val	
20 25 30	
aag cct gga ggg tcc ctg aaa ctc tcc tgt gca gcc gct gga ttc act	146
Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Gly Phe Thr	
35 40 45	
ttc agt aga tat gcc atg tct tgg gtt cgc cag act ccg gag aag agg	194
Phe Ser Arg Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg	
50 55 60	
ctg gag tgg gtc gca acc ata agt agt ggt agt agt cac acc tac tat	242
Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser His Thr Tyr Tyr	
65 70 75	
cca gac agt gtg aag ggg cga ttc acc atc tcc aga gac aat gcc aag	290
Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys	
80 85 90 95	
aac acc ctg tac ctg caa atg agc agt ctg agg tct gag gac acg gcc	338
Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala	
100 105 110	
ata tat tac tgt gca aga ccg ggt tac gac agg ggg gcc tgg ttt ttc	386
Ile Tyr Tyr Cys Ala Arg Pro Gly Tyr Asp Arg Gly Ala Trp Phe Phe	
115 120 125	
gat gtc tgg ggc gca ggg acc acg gtc acc gtc tcc tca ggtaagtgtg	435
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser	
130 135 140	

tcagggtttc acaagaggga ctaaagacat gtcagcta at gtgtgactaa tggtaatgtc 495  
 actaagctt 504

<210> 4  
 <211> 140  
 <212> PRT  
 <213> Mus sp.

<400> 4

Met Asn Phe Gly Phe Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly  
 1 5 10 15

Val Gln Cys Glu Val Val Val Glu Ser Gly Gly Gly Phe Val Lys  
 20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ala Gly Phe Thr Phe  
 35 40 45

Ser Arg Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu  
 50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser His Thr Tyr Tyr Pro  
 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile  
 100 105 110

Tyr Tyr Cys Ala Arg Pro Gly Tyr Asp Arg Gly Ala Trp Phe Phe Asp  
 115 120 125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser  
 130 135 140

<210> 5  
<211> 483  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (16)..(399)  
<223> MB3.6 Light chain V region, plus leader

<400> 5	51
agggaaagct cgaag atg gtt ttc aca cct cag ata ctt gga ctt atg ctt	
Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu	
1 5 10	
ttt tgg att tca gcc tcc aga ggt gat att gtg cta act cag tct cca	99
Phe Trp Ile Ser Ala Ser Arg Gly Asp Ile Val Leu Thr Gln Ser Pro	
15 20 25	
gcc acc ctg tct gtg act cca gga gat agc gtc agt ctt tcc tgc agg	147
Ala Thr Leu Ser Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg	
30 35 40	
gcc agc caa att att agc aac aac cta cac tgg tat caa caa aaa tca	195
Ala Ser Gln Ile Ile Ser Asn Asn Leu His Trp Tyr Gln Gln Lys Ser	
45 50 55 60	
cat gag tct cca agg ctt ctc atc aag tat gct tcc cag tcc atc tct	243
His Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser	
65 70 75	
ggg atc ccc tcc agg ttc agt ggc agt gga tca ggg aca gat ttc act	291
Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr	
80 85 90	
ctc agt atc aac agt gtg gag act gaa gat ttt gga atg tat ttc tgt	339
Leu Ser Ile Asn Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys	
95 100 105	
caa cag agt aac agc tgg cct ctc acg ttc ggc tcg ggg aca aag ctg	387
Gln Gln Ser Asn Ser Trp Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu	
110 115 120	
gag atc aaa cgg cgtaagtgtg tcagggtttc acaagaggga ctaaagacat	439
Glu Ile Lys Arg	
125	

gtcagctaat gtgtgactaa tggtaatgtc acttgcagg atcc

483

<210> 6  
<211> 128  
<212> PRT  
<213> Mus sp.

&lt;400&gt; 6

Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu Phe Trp Ile Ser  
1 5 10 15

Ala Ser Arg Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser  
20 25 30

Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ile  
35 40 45

Ile Ser Asn Asn Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro  
50 55 60

Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser  
65 70 75 80

Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn  
85 90 95

Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn  
100 105 110

Ser Trp Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg  
115 120 125

<210> 7  
<211> 258  
<212> DNA  
<213> Mus sp.

&lt;220&gt;

```

<221> misc_feature
<222> (1)..(258)
<223> Light chain leader plus sFv of MB3.6

<400> 7
gatatcagat ctcagctgtc tagacatatg gtttcacac ctcagatann nnnnnnnnnn 60
nnnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnngggac aaagctggag 120
atcaaaggta gctcaggatc ggggtggagcc ggctctggtg gctcaggatc ggaagtggtg 180
gtgggtggagn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnacc 240
acggtcaccg tctccagt 258

<210> 8
<211> 682
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (20)..(418)
<223> 3D8 Heavy chain V region, plus leader

<400> 8
tgaacacgga cccctcacc atg aac ttc ggg ctc agc ttg att ttc ctt gtc 52
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val
1 5 10
ctt gtt tta aaa ggt gtc cag tgt gaa gta aag gtt gtt gag tct ggg 100
Leu Val Leu Lys Gly Val Gln Cys Glu Val Lys Val Val Glu Ser Gly
15 20 25
gga ggc tta gtg aag cct gga gcg tct ctg aaa ctc tcc tgt gca gcc 148
Gly Gly Leu Val Lys Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala
30 35 40
tct gga ttc act ttc agt aac tat ggc atg tct tgg gtt cgc cag act 196
Ser Gly Phe Thr Phe Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr
45 50 55
tca gac aag agg ctg gag tgg gtc gca tcc att agt agt ggt ggt gat 244
Ser Asp Lys Arg Leu Glu Trp Val Ala Ser Ile Ser Ser Gly Gly Asp
60 65 70 75

```

agc acc ttc tat gca gac aat gta aag ggc cga ttc acc atc tcc aga	292	
Ser Thr Phe Tyr Ala Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg		
80	85	90
gag aat gcc aag aac acc ctg tac ctg caa atg agt agt ctg aag tct	340	
Glu Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser		
95	100	105
gag gac acg gcc ttg tat tac tgt gca aga gac gat cta ttt aac tgg	388	
Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Asp Asp Leu Phe Asn Trp		
110	115	120
ggc caa ggc acc act ctc aca gtc tca tca gccaaaacaa cagccccatc	438	
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser		
125	130	
ggtctatcca ctggccctg tgtgtggaga tacaattggc tcctcggtga ctttaggatg	498	
cctggtcaag ggttatttcc ttgagccagt gaccttgacc tggaactctg gatccctgtc	558	
cagtggtgtg cacatcttcc cagctgtctt gcagtctgac ctctacaccc tcagcagctc	618	
agtgactgta acctcgagca cctggccag ccagtccatc acttgcaatg tggcccaccc	678	
ggca	682	

<210> 9  
 <211> 133  
 <212> PRT  
 <213> Mus sp.

<400> 9  
 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly  
 1 5 10 15

Val Gln Cys Glu Val Lys Val Val Glu Ser Gly Gly Leu Val Lys  
 20 25 30

Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45

Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu

50

55

60

Glu Trp Val Ala Ser Ile Ser Ser Gly Gly Asp Ser Thr Phe Tyr Ala  
 65 70 75 80

Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn  
 85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu  
 100 105 110

Tyr Tyr Cys Ala Arg Asp Asp Leu Phe Asn Trp Gly Gln Gly Thr Thr  
 115 120 125

Leu Thr Val Ser Ser  
 130

<210> 10  
 <211> 729  
 <212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (15)..(410)  
 <223> 3D8 Light chain V region, plus leader

<400> 10	50
ccgttgcgt cgtg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc	
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu	
1 5 10	
tgg att cag gaa acc aac ggt gat gtt gta atg acc cag act cca ctc	98
Trp Ile Gln Glu Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu	
15 20 25	
act ttg tcg gtt acc att gga caa cca gcc tct atc tct tgc aag tca	146
Thr Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser	
30 35 40	
agt cag agc ctc tta tat agt aat gga aaa acc tat ttg aat tgg tta	194

Ser Gln Ser Leu Leu Tyr Ser Asn Gly Lys Thr Tyr Leu Asn Trp Leu	55	60	
45	50		
tta cag agg cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct			242
Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser			
65	70	75	
aaa ctg gac tct gga gtc cct gac agg ttc act ggc agt gga tca gga			290
Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly			
80	85	90	
aca gat ttt aca ctg aaa atc agc aga gtg gag gct gag gat ttg gga			338
Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly			
95	100	105	
gtt tat tac tgc gtg caa ggt aca cat ttt cct cac acg ttc gga ggg			386
Val Tyr Tyr Cys Val Gln Gly Thr His Phe Pro His Thr Phe Gly Gly			
110	115	120	
ggg acc aag ctg gaa ata aaa cgg gctgatgctg caccaactgt atccatcttc			440
Gly Thr Lys Leu Glu Ile Lys Arg			
125	130		
ccaccatcca gtgagcagtt aacatctgga ggtgcctcag tcgtgtgctt cttgaacaac			500
ttctacccca aagacatcaa tgtcaagtgg aagattgatg gcagtgaacg acaaaatggc			560
gtcctgaaca gttggactga tcaggacagc aaagacagca cctacagcat gagcagcacc			620
ctcacgttga ccaaggacga gtatgaacga cataacagct atacctgtga ggccactcac			680
aagacatcaa cttcacccat tgtcaagacg ttcaacagga atgagtgtt			729

<210> 11  
 <211> 132  
 <212> PRT  
 <213> Mus sp.

<400> 11

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Gln Glu			
1	5	10	15

Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val			
20	25	30	

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu  
 35 40 45

Leu Tyr Ser Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro  
 50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser  
 65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys  
 100 105 110

Val Gln Gly Thr His Phe Pro His Thr Phe Gly Gly Thr Lys Leu  
 115 120 125

Glu Ile Lys Arg  
 130

<210> 12

<211> 736

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (14)..(430)

<223> 4D4 Heavy chain V region, plus leader

<400> 12

actgactcta acc atg gga tgg aga tgg atc ttt ctt ttc ctc ctg tca  
 Met Gly Trp Arg Trp Ile Phe Leu Phe Leu Leu Ser  
 1 5 10

49

gga act gca ggt gtc cat tgc cag gtt cag ctg cag cag tct gga cct  
 Gly Thr Ala Gly Val His Cys Gln Val Gln Leu Gln Ser Gly Pro  
 15 20 25

97

gag ctg gtg aag cct ggg gct tta gtg aag ata tcc tgc aag gct tct	145
Glu Leu Val Lys Pro Gly Ala Leu Val Lys Ile Ser Cys Lys Ala Ser	
30 35 40	
ggt tac acc ttc aca agc tac gat ata aac tgg gtg aag cag agg cct	193
Gly Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln Arg Pro	
45 50 55 60	
gga cag gga ctt gag tgg att gga tgg att tat cct gga gat ggt ggt	241
Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Gly	
65 70 75	
act aat tac aat gag aaa ttc aag ggc aag gcc aca ctg act gca gac	289
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp	
80 85 90	
aaa tcc tcc agc aca gcc tac atg cag ctc agt agc ctg act tct gag	337
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu	
95 100 105	
aac tct gca gtc tat ttc tgt gca aga ggg ggt aac ttc cct tct tat	385
Asn Ser Ala Val Tyr Phe Cys Ala Arg Gly Gly Asn Phe Pro Ser Tyr	
110 115 120	
gct atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca	430
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser	
125 130 135	
gcacaaaacga cacccccatac tgtctatcca ctggcccttg gatctgctgc ccaaactaac	490
tccatggta ccccggtatg cctggtaag ggctatttcc ctgagccagt gacagtgacc	550
tggaaactctg gatccctgtc cagcggtgtg cacaccccttcc cagctgtcct gcagtctgac	610
ctctacactc tgagcagctc agtgactgtc ccctccagca cctggccctag cgagaccgtc	670
acctgcaacg ttgcccaccc ggccagcagc accaagggtgg acaagaaaat tgtgcccagg	730
736	
gattgt	

<210> 13  
 <211> 139  
 <212> PRT  
 <213> Mus sp.

<400> 13

Met Gly Trp Arg Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly  
 1 5 10 15  
 Val His Cys Gln Val Gln Leu Gln Ser Gly Pro Glu Leu Val Lys  
 20 25 30  
 Pro Gly Ala Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
 50 55 60  
 Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Gly Thr Asn Tyr Asn  
 65 70 75 80  
 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
 85 90 95  
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val  
 100 105 110  
 Tyr Phe Cys Ala Arg Gly Gly Asn Phe Pro Ser Tyr Ala Met Asp Tyr  
 115 120 125  
 Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
 130 135

<210> 14  
 <211> 504  
 <212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (7)..(402)  
 <223> 4D4 Light chain V region, plus leader

<400> 14		48
ctcaaa atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att		
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile		
1 5 10		
cct gct tcc aac agt gat gtt ttg atg acc caa tct cca ctc tcc ctg		96
Pro Ala Ser Asn Ser Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu		
15 20 25 30		
cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag		144
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln		
35 40 45		
agc att gtc cat agt aat gga gac acc tat tta gaa tgg tac ctg cag		192
Ser Ile Val His Ser Asn Gly Asp Thr Tyr Leu Glu Trp Tyr Leu Gln		
50 55 60		
aaa cca ggc cag tct cca aag ctc ctg atc tac aag gtt tcc gac cga		240
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asp Arg		
65 70 75		
ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat		288
Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp		
80 85 90		
ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat		336
Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr		
95 100 105 110		
ttc tgc ttt caa ggt tca cat gtt ccg tac gcg ttc gga ggg ggg acc		384
Phe Cys Phe Gln Gly Ser His Val Pro Tyr Ala Phe Gly Gly Thr		
115 120 125		
aag ctg gaa ata aaa cgg gctgatgctg caccaactgt atccatcttc		432
Lys Leu Glu Ile Lys Arg		
130		
ccaccatcca gtgagcagtt aacatctgga ggtgcctcag tcgtgtgctt cttgaacaac		492
ttctacccca aa		504

<210> 15  
<211> 132  
<212> PRT  
<213> Mus sp.

<400> 15

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala  
1 5 10 15

Ser Asn Ser Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro Val  
20 25 30

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile  
35 40 45

Val His Ser Asn Gly Asp Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro  
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asp Arg Phe Ser  
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr  
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys  
100 105 110

Phe Gln Gly Ser His Val Pro Tyr Ala Phe Gly Gly Thr Lys Leu  
115 120 125

Glu Ile Lys Arg  
130

<210> 16  
<211> 761  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (62)..(478)  
<223> 3E11 Heavy chain V region, plus leader

<400> 16 cctggattca atttccagtt cctcacattc agtgatcagc actgaacacg gaccctcac 60  
 c atg aac ttc ggg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt 109  
 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly  
 1 5 10 15  
 gtc cag tgt gaa gtg aaa ctg gtg gag tct ggg gga gac tta atg aac 157  
 Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Asp Leu Met Asn  
 20 25 30  
 cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc agt ttc 205  
 Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe  
 35 40 45  
 agt aac tat ggc atg tct tgg gtt cgc cag act tca gac aag agg ctg 253  
 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu  
 50 55 60  
 gag tgg gtc gct tcc att agt acg ggt ggt gct aat acc ttc tat cca 301  
 Glu Trp Val Ala Ser Ile Ser Thr Gly Gly Ala Asn Thr Phe Tyr Pro  
 65 70 75 80  
 gac aat gta aag ggc cga ttc acc att tcc aga gag aat gcc aag aac 349  
 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn  
 85 90 95  
 acc cta tac ctg caa atg agt ctg aag tct gag gac acg gcc ttg 397  
 Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu  
 100 105 110  
 tat ttc tgt gca aga gat agt cac tcc gta ggt tgt tgg ttt gct acc 445  
 Tyr Phe Cys Ala Arg Asp Ser His Ser Val Gly Cys Trp Phe Ala Thr  
 115 120 125  
 tgg ggc caa ggg act ctg gtc act gtc tct gca gccaaaacaa caccctcac 498  
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala  
 130 135  
 agtctatcca ctggccctg ggtgtggaga tactactggc tcctccgtga ctctggatg 558  
 cctggtaag ggctacttcc ctgagtcagt gactgtgact tggaactccg gatccctgcc 618  
 cagcagtgtg cacaccttc cagctctcc gcagtcgtt ctctacacta tgagcagctc 678  
 agtgactgtc ccctccagca cctggccaag ccagaccgtt acctgcgtt ttgctcaccc 738  
 agccagcagc accacgggtgg aca 761

<210> 17  
 <211> 139  
 <212> PRT  
 <213> Mus sp.

<400> 17

Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly  
 1 5 10 15

Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Asp Leu Met Asn  
 20 25 30

Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe  
 35 40 45

Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu  
 50 55 60

Glu Trp Val Ala Ser Ile Ser Thr Gly Gly Ala Asn Thr Phe Tyr Pro  
 65 70 75 80

Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn  
 85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu  
 100 105 110

Tyr Phe Cys Ala Arg Asp Ser His Ser Val Gly Cys Trp Phe Ala Thr  
 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala  
 130 135

<210> 18  
 <211> 698  
 <212> DNA

&lt;213&gt; Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (6)..(401)

&lt;223&gt; 3E11 Light chain V region, plus leader

<400>	18	50
ccagc	atg ggc atc aag atg gaa tca cag act ctg gtc ttc ata tcc ata	
Met	Gly Ile Lys Met Glu Ser Gln Thr Leu Val Phe Ile Ser Ile	
1	5 10 15	
ctg	ctc tgg tta tat gga gct gat ggg aac att gta atg acc caa tct	98
Leu	Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser	
20	25 30	
ccc	aaa tcc atg tcc atg tca gta gga gag agg gtc acc ttg acc tgc	146
Pro	Lys Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys	
35	40 45	
aag	gcc agt gag aat gtg gtt act tat gtt tcc tgg tat caa cag aaa	194
Lys	Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys	
50	55 60	
cca	gag cag tct cct aaa ctg ctg ata tac ggg gca tcc aac cgg tac	242
Pro	Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr	
65	70 75	
act	ggg gtc ccc gat cgc ttc aca ggc agt gga tct gca aca gat ttc	290
Thr	Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe	
80	85 90 95	
act	ctg acc atc agc agt gtg cag gct gaa gac ctt gca gat tat cac	338
Thr	Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His	
100	105 110	
tgt	gga cag ggt tac agc tat ccg tac acg ttc gga ggg ggg acc aag	386
Cys	Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Thr Lys	
115	120 125	
ctg	gaa ata aaa cgg gctgatgctg caccaactgt atccatcttc ccaccatcca	441
Leu	Glu Ile Lys Arg	
130		
gtgagcagtt	aacatctgga ggtgcctcag tcgttgctt cttgaacaac ttctacccca	501
aagacatcaa	tgtcaagtgg aagattgatg gcagtgaacg acaaaatggc gtcctgaaca	561

gttggactga tcaggacagc aaagacagca cctacagcat gagcagcacc ctcacgttga 621  
 ccaaggacga gtagaacga cataacagct atacctgtga ggccactcac aagacatcaa 681  
 698  
 cttcacccat cgtcaag

<210> 19  
 <211> 132  
 <212> PRT  
 <213> Mus sp.

<400> 19  
 Met Gly Ile Lys Met Glu Ser Gln Thr Leu Val Phe Ile Ser Ile Leu  
 1 5 10 15  
 Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro  
 20 25 30

Lys Ser Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys  
 35 40 45  
 Lys Ser Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys

Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro  
 50 55 60

Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr  
 65 70 75 80  
 Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr  
 85 90 95  
 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr

Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys  
 100 105 110  
 Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys

Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu  
 115 120 125  
 Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Thr Lys Leu

Glu Ile Lys Arg

Ant dies as Chimeric Effector C11.ST25

130